

20250303 09:26:00

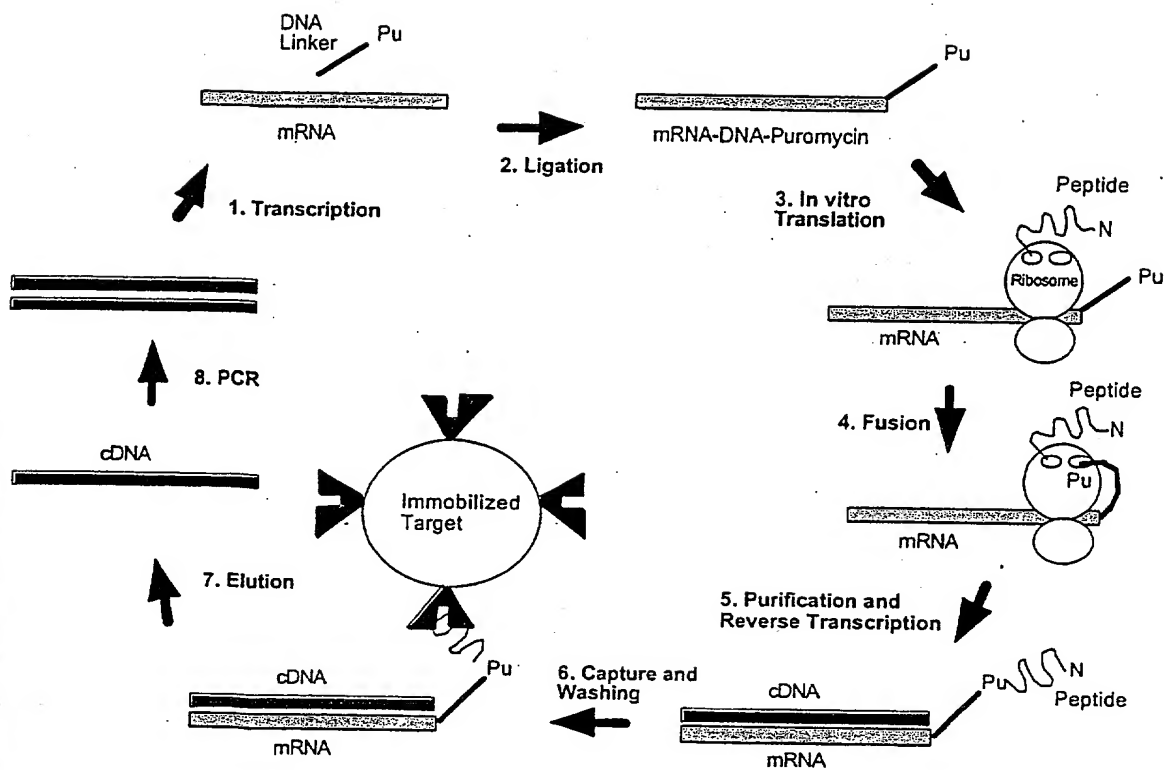


FIGURE 1

A.

Bcl-2										M	P	V	V	H	L	T	L	T	T	A	G	D	D	F	S	R	R
Bax	M	P	Q	D	A	S	T	K	K	L	S	E	C	L	K	R	I	G	D	E	L	D	S	N	G		
Bak											M	G	Q	V	G	R	Q	L	A	I	I	G	D	D	I	N	

B.

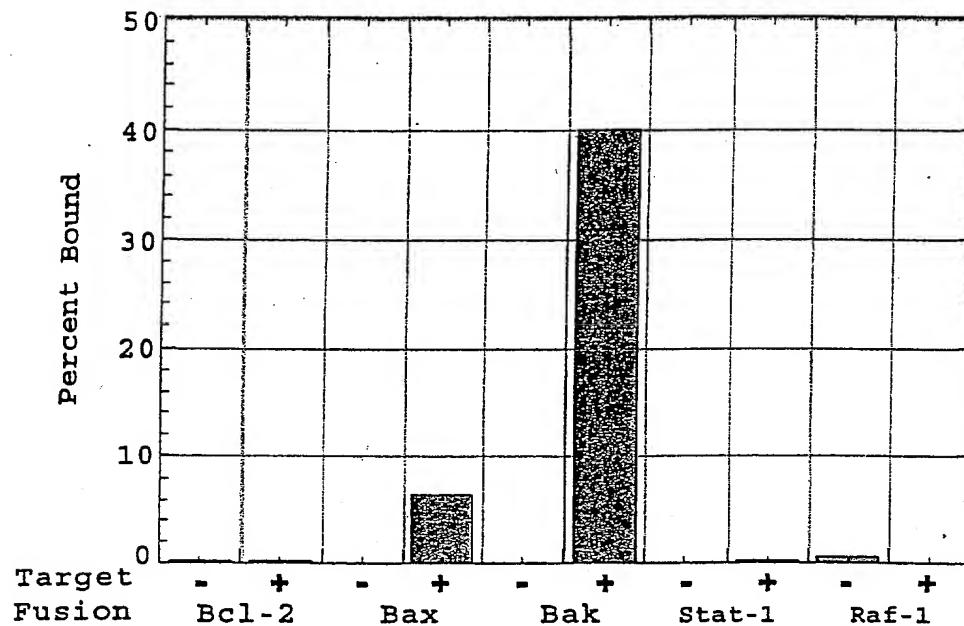


FIGURE 2

204080-0522600T

Number	Protein Name	Accession numbers	Clone	Protein Sequence	Kd	R value	GST Binding Percent	BaBPH3 (μM)	BaBPH3 effect	Kidney	Liver	Marrow	Total
1	Bim	NP 005529.1	144	ASMRGAEPADMRPEWIAQELRRIGDFNAYARE	0.0019	0.97	0.3	100	0.94	42	11	36	89
2	Bak	NP 001179.1	C32	GVGRLAIGDINRRK	0.402	0.98	0.2	20	0.36	19	2	1	22
3	Bax	NP 004315.1	C49	TKSECLRLGDELLEAEVINGLQMAVDTDSPR	0.76	0.99	0.4	20	ND	0	0	0	0
4	Bcl2 L12	AF289220.1	775	KGSEALRLVALLSEAEVINGLQMAVDTDSPR	0.42	0.99	0.4	20	ND	0	0	0	0
5	Neurotrophin cytosolic factor 2	NP 004241.1	192	GGEDYDYTEKYDAIKDLKALIGLQGN	0.00416	0.92	0.3	20	0.66	0	0	0	0
6	Talin (splice variant)	NP 002680.1	X56	GGEDYDYTEKYDAIKDLKALIGLQGN	0.093	0.98	0.8	20	0.21	4	0	0	4
7	Gq1i SNAP receptor complex member 1	NP 004862.1	X06	GGEDYDYTEKYDAIKDLKALIGLQGN	0.467	0.94	0.1	20	0.12	0	0	0	0
8	HSCP300	AF161418	C68	AYQDPVQREIHDWNRVETIITSKIKAD	0.58	0.97	0.8	20	0.21	9	15	11	35
9	Syntaxin 4A	NP 004595.1	U58	ATQALNEISARHGQIQERSIEHLDIFFL	0.64	0.88	0.4	20	0.14	8	4	0	12
10	Tumor protein HDMC21P	NP 003286.1	U50	FWLEEDYQREIHDWNRVETIITSKIKAD	0.69	0.98	1.3	20	0.18	1	5	5	11
11	Toll-like receptor 3	NP 003286.1	U15	FWLEEDYQREIHDWNRVETIITSKIKAD	1.12	0.98	0.3	20	0.07	4	0	0	4
12	Voltage dependent anion channel 3	NP 005653.1	X02	RGAVSQDKVQVQATKVLNRADNFINDR	2.5	0.99	0.1	20	0.32	0	0	0	0
13	Adipocyte dehydrogenase	NP 003739.1	X05	TGTAPEAFKEQELNSALHSDLDIOTITLP	2.75	0.99	0.2	20	0.08	3	0	0	3
14	Human retrotransposon L1	P06847	C55	SNELTRAVELEKLLKARE	4.46	0.97	0.4	20	0.16	23	0	0	23
15	TPR nuclear pore complex-associated protein	NP 003283.1	U25	TYNNLLPPAPRIKEVLTDFAKVLEKGVDSRS	5.24	0.98	0.3	20	0.09	5	0	0	5
16	TRAP100 Thyroid hormone receptor-associated protein	NP 003855.1	C56	FTILLTLLMRCSPSPG	7.5	0.98	0.3	20	0.19	1	1	0	2
17	Parathyroid hormone receptor	NP 003316.1	C56	FTILLTLLMRCSPSPG	9.6	0.91	0.2	20	0.08	0	0	0	0
18	Chaperon	NP 002529.1	X33	GLRESEVSEKELTILNRIISKHKLRT	8.2	0.96	0.3	20	0.02	0	0	0	0
19	Octadecan, light junction protein	NP 004832.1	C26	KGILSERVSEELKRDHAEAGCGQLEDHLMRPSAFASLDVAVNARIWSALT PAXRVVXHCX	PD	0.91	0.2	20	0.05	0	0	0	0
20	Human p64 protein	NP 001139.2	X69	WERLEERLAIADHLGFSWTELRAL	PD	0.91	0.2	20	0.05	0	0	0	0
21	Myrin 2	NP 004167.2	X17	ARGDFAQAQQLWALRALGRPLTSH	PD	0.91	0.2	20	0.05	0	0	0	0
22	Bleed regulatory element binding factor (splice variant)	NP 004637.1	X49	GSGLAKHQVQVGDMDLTPKHDLKPQC	PD	0.91	0.2	20	0.05	0	0	0	0
23	Dicacylglycerol kinase Zeta	NP 004637.1	X49	GSGLAKHQVQVGDMDLTPKHDLKPQC	PD	0.91	0.2	20	0.05	0	0	0	0
24	Translin	NP 004637.1	X49	GSGLAKHQVQVGDMDLTPKHDLKPQC	PD	0.91	0.2	20	0.05	0	0	0	0
25	Hep C associated interferon-induced microtubulin	NP 006408.1	X53	LDPAKVDILSALRMMAWADDFEELPFEOIG	5.04	0.95	1.4	20	0.79	1	1	0	2
26	Mitochondrial NADH dehydrogenase subunit 1	NP 008342.1	C27	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
27	Mitochondrial ATP synthase F0 subunit 8	NP 008342.1	C27	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
28	Mitochondrial NADH dehydrogenase chain 5	NP 008342.1	C27	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
29	Hypothetical protein DKF2P5434e171	AL11795	X16	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
30	Hypothetical protein DKF2P5662124	AL11758.1	X16	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
31	Hypothetical protein KIAA1501	AB040934.1	X72	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
32	Hypothetical protein DKF2P5860623	NM_017540.1	X37	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
33	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
34	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
35	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
36	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
37	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
38	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
39	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
40	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
41	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
42	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
43	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
44	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
45	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
46	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
47	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
48	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
49	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
50	Unknown protein from cDNA: FLJ21691	AK025344.1	X42	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
51	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
52	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
53	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
54	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
55	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
56	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
57	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
58	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
59	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
60	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
61	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
62	Sequence/protein not in database	AI 359079	C39	LVKLLVMPVLLMAELMTLTKILGYIQPR	PD	0.95	1.4	20	0.77	1	1	0	2
63	Proline/glutamine rich splicing factor (out of frame)	NP 005065	C83	RGLVVDRLVEEWLEPRQ	2.23	0.98	0.7	20	0.07	2	0	0	2
64	Transforming growth factor (reversed orientation)	NP 003758	X84	FVRSVGWRLGIDMDMDHAIHGCHDVRIG	1.61	0.92	0.8	20	0.26	3	0	0	3
65	Lipidase (3' UTR)	NP 002298	X67	SSGLKPTIGSSOR	4.51	0.93	0.1	20	0.36	1	0	0	1
66	Arsenite resistance protein (reversed orientation)	NP 002298	X67	SSGLKPTIGSSOR	4.51	0.93	0.1	20	0.36	1	0	0	1
67	K-Ras oncogene (3' UTR)	NP 015908	X93	AGTQKPLAOFMRVGGDELLHFLW	PD	0.87	0.4	20	0.48	0	0	0	0
68	Lysosomal peptidase (3' UTR)	NP 004985	X91	MDTKGLDGLTFQVADALISLLPPLAIA	PD	0.87	0.4	20	0.48	0	0	0	0
69	MyBPC3 (3' UTR)	NP 000256	C41	ATYMKTLQGLLOQVAPSSSH	0.07	0.89	1.4	20	0.44	3	0	0	3
70	cDNA FL20617 (not in predicted OR)	AK006624	C4	GSLLHHNNINPSSIR	0.086	0.93	2.5	20	0.37	1	11	6	18
71	UDP-glucuronosyl transferase 2B4 precursor (out of frame)	NP 003548	X90	VSCWPSYKLPKSTASASLATQKSLA	PD	0.93	2.1	20	ND	0	0	0	0

PD = Poorly determined, ND = Not Determined, NB = Not Binding, * = High background binding

FIGURE 3B

SEQ ID NO 1: BimL (Corresponds to the nucleic acid sequence of SEQ ID NO: 153)
A S M R Q A E P A D M R P E I W I A Q E L R R I G D E F N A Y Y A R E

SEQ ID NO: 2 Bak (Corresponds to the nucleic acid sequence of SEQ ID NO: 154)
G Q V G R Q L A I I G D D I N R R K

SEQ ID NO: 3 Bax (Corresponds to the nucleic acid sequence of SEQ ID NO: 155)
K L S E C L K R I G D E L D S N M E L Q R M I A A V D T D S P R

SEQ ID NO: 4 Bcl2 L12 (Corresponds to the nucleic acid sequence of SEQ ID NO: 156)
T G K E A I L R R L V A L L E E E A E V I N Q K L A S D P A L R S K L V R L S S D S F A
H L

SEQ ID NO: 5 Neutrophil cytosolic factor 2 (Corresponds to the nucleic acid sequence of SEQ ID NO: 157)
Q R G M L Y Y Q T E K Y D L A I K D L K E A L I Q L R G N N

SEQ ID NO: 6 Talin (splice variant) (Corresponds to the nucleic acid sequence of SEQ ID NO: 158)
G G E S D T D P H F Q D A L M Q L A K A V A S A A A A L V L K A K S V A Q R

SEQ ID NO: 7 Golgi SNAP receptor complex member 1 (Corresponds to the nucleic acid sequence of SEQ ID NO: 159)
G T R Q D R M F E T M A I E I E Q L L A R L T G V N D K M A E Y T N A

SEQ ID NO: 8 HSCP300 (Corresponds to the nucleic acid sequence of SEQ ID NO: 160)
A V Q E D P V Q R E I H Q D W A N R E Y I E I T S S I K K I A D

SEQ ID NO: 9 Syntaxin 4A (Corresponds to the nucleic acid sequence of SEQ ID NO: 161)
A T R Q A L N E I S A R H S G I Q Q L E R S I R E L H D I F T F L

SEQ ID NO: 10 Tumor protein HDCMB21P (Corresponds to the nucleic acid sequence of SEQ ID NO: 162)
M F S D I Y G I R E I A D G L C L E V E G K M V S R P E

SEQ ID NO: 11 Toll-like receptor 3 (Corresponds to the nucleic acid sequence of SEQ ID NO: 163)
F W L E E R D F E A G V F E L E A I V N S I K R S

SEQ ID NO: 12 Voltage dependent anion channel 3 (Corresponds to the nucleic acid sequence of SEQ ID NO: 164)
M K W D T D N T L G T E I S W E N K L A E G L K L T L D T I F V H H V L H A P H

FIGURE 3B

SEQ ID NO: 13 Aldehyde dehydrogenase (Corresponds to the nucleic acid sequence of SEQ ID NO: 165)

R G A V F S Q D K D V V Q E A T K V L R N A A D N F Y I N D R

SEQ ID NO: 14 Human retrotransposon L1 (Corresponds to the nucleic acid sequence of SEQ ID NO: 166)

T G T G A P R F I K E V Q E L N S A L H Q S D L I D I Y R T L H P

SEQ ID NO: 15 TPR, nuclear pore complex-associated protein (Corresponds to the nucleic acid sequence of SEQ ID NO: 167)

S N E L T R A V E E L H K L L K E A R E

SEQ ID NO: 16 TRAP100 Thyroid hormone receptor-associated protein (Corresponds to the nucleic acid sequence of SEQ ID NO: 168)

T Y W N L L P P K R P I K E V L T D I F A K V L E K G W V D S R S

SEQ ID NO: 17 Parathyroid hormone receptor (Corresponds to the nucleic acid sequence of SEQ ID NO: 169)

L F T I L L T L W T M R C S S T P S G

SEQ ID NO: 18 Calpain (Corresponds to the nucleic acid sequence of SEQ ID NO: 170)

A G E D M E I S V K E L R T I L N R I I S K H K D L R T

SEQ ID NO: 19 Occludin, tight junction protein (Corresponds to the nucleic acid sequence of SEQ ID NO: 171)

G L R E E S E E Y M A A A D E Y N R L K Q V K Q P A

SEQ ID NO: 20 Human nGAP protein (Corresponds to the nucleic acid sequence of SEQ ID NO: 172)

K G I I S R L M S V E E E L K R D H A E M Q A G C G L Q T E D H L M P R R S A F A S L
D A V N A R L M S A L T P A X R Y V X H C X P L

SEQ ID NO: 21 Ankryn 2 (Corresponds to the nucleic acid sequence of SEQ ID NO: 173)

W E R I E E R L A Y I A D H L G F S W T E L A R A L

SEQ ID NO: 22 Sterol regulatory element binding txn factor (splice variant) (Corresponds to the nucleic acid sequence of SEQ ID NO: 174)

A R G D F A Q A A Q Q L W L A L R A L G R P L P T S H

SEQ ID NO: 23 Diacylglycerol kinase Zeta (Corresponds to the nucleic acid sequence of SEQ ID NO: 175)

G S S K D L A K H I Q V V C D G M D L T P K I H D L K P Q C

FIGURE 3B

SEQ ID NO: 24 Translin (Corresponds to the nucleic acid sequence of SEQ ID NO: 176)
GFLAAEQDIREERKVVQSLEQTAREVLTLLQG

SEQ ID NO: 25 Hep C associated,interferon-induced microtubular (Corresponds to the nucleic acid sequence of SEQ ID NO: 177)
LDPVKDVLILSALRRMLWAADDFLEDLPFEQIG

SEQ ID NO: 26 Mitochondrial NADH dehydrogenase subunit 1 (Corresponds to the nucleic acid sequence of SEQ ID NO: 178)
ANLLLLMVPILIAMAFMLTERKILGYIQPR

SEQ ID NO: 27 Mitochondrial ATP synthase F0 subunit 8 (Corresponds to the nucleic acid sequence of SEQ ID NO: 179)
LRLNTTVWPTIITPILLTLFLITNRLITTR

SEQ ID NO: 28 Mitochondrial NADH dehydrogenase chain 5 (Corresponds to the nucleic acid sequence of SEQ ID NO: 180)
TLYLKLTALAVTFLGLLTALDLNYPT

SEQ ID NO: 29 Hypothetical protein DFKZp434e171 (Corresponds to the nucleic acid sequence of SEQ ID NO: 181)
AGVFS AEPSPFPQTRRSMVFARHLREVGDEFRRSRHLNSTDDAD
E

SEQ ID NO: 30 Hypothetical protein DKFZp566f2124 (Corresponds to the nucleic acid sequence of SEQ ID NO: 182)
GLKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAET
T

SEQ ID NO: 31 Hypothetical protein KIAA1501 (Corresponds to the nucleic acid sequence of SEQ ID NO: 183)
MRDLP GHYYETLKFLVGHLKTIADHR

SEQ ID NO: 32 Hypothetical protein DKFZp586ho623 (Corresponds to the nucleic acid sequence of SEQ ID NO: 184)
CGGRMEDIPCSRVGHIYRKYPYKVPAGVSLARNLKRVDWM

SEQ ID NO: 33 unknown protein from cDNA: FLJ21691 fis, clone COL09555 (Corresponds to the nucleic acid sequence of SEQ ID NO: 185)
ALSWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCAHP

FIGURE 3B

SEQ ID NO: 34 unknown protein from Mitochondrial DNA (Corresponds to the nucleic acid sequence of SEQ ID NO: 186)

TSTLPHIRRT R

SEQ ID NO: 35 Unknown protein from Homo sapiens cDNA: FLJ23277 fis, clone HEP03322 (Corresponds to the nucleic acid sequence of SEQ ID NO: 187)

NGNLFASFIA DS

SEQ ID NO: 36 unknown protein from Homo sapiens cDNA: FLJ22171 fis, clone HRC00654 (Corresponds to the nucleic acid sequence of SEQ ID NO: 188)

ILTSPTTSSGLWPRLQKAAEAFKQLNQ P

SEQ ID NO: 37 unknown protein from cDNA FLJ23179 fis, clone LNG10890 (Corresponds to the nucleic acid sequence of SEQ ID NO: 189)

RTLQPRLLQNQQQHLPALPIWFLLQWLRLHPL

SEQ ID NO: 38 unknown protein from clone RP5-889J22 on chromosome 22q13.1 (Corresponds to the nucleic acid sequence of SEQ ID NO: 190)

MAVIINELSQRDSCGPLKISLNNKILVYGNLFSSTP

SEQ ID NO: 39 Unknown protein from Mitochondrial DNA (Corresponds to the nucleic acid sequence of SEQ ID NO: 191)

GLAKKSKRNPANLTPP

SEQ ID NO: 40 Unknown protein from Homo sapiens chromosome X (Corresponds to the nucleic acid sequence of SEQ ID NO: 192)

SSQALRIHQWLHLFSDFTST

SEQ ID NO: 41 unknown protein bfrom clone RP11-141E20 on chromosome 1q31.2-31.3 (Corresponds to the nucleic acid sequence of SEQ ID NO: 193)

GQVGRQLAIIIGDDINRRK

SEQ ID NO: 42 unknown protein from chromosome 21q22.2, cosmid clone:D37D12, CBR1-HLCS region (Corresponds to the nucleic acid sequence of SEQ ID NO: 194)

GVSEAEGETFPLSTFLLGIASRLRSVA

SEQ ID NO: 43 Unknown protein from Homo sapiens clone RP11-198M19, homology to retrotransposon (Corresponds to the nucleic acid sequence of SEQ ID NO: 195)

RAPRFIKQILLDLKREIDFNVRLVEYFNPLS

FIGURE 3B

SEQ ID NO: 44 Unknown protein with RNA Homology to Murine retrovirus readthrough seq.
(Corresponds to the nucleic acid sequence of SEQ ID NO: 196)

I V A I I A G R L R M L G D Q F N G E L E A S A K N

SEQ ID NO: 45 Unknown protein from CpG island (Corresponds to the nucleic acid sequence
of SEQ ID NO: 197)

L A L A Y Y S S R Q Y A S A L K H I A E I I E R G I R Q H

SEQ ID NO: 46 unknown protein from clone 425C14 on chromosome 6q22 (Corresponds to the
nucleic acid sequence of SEQ ID NO: 198)

A A M L L D R R G T E C D L W I N E M S L L H K I V Q D V Y G T P H P P H S

SEQ ID NO: 47 unknown protein from Human genomic DNA of Xq28 with MTM1 and
MTMR1 genes (Corresponds to the nucleic acid sequence of SEQ ID NO: 199)

P W Q Y K P I A D L Y R G R E S R P S A P R

SEQ ID NO: 48 unknown protein from clone RP11-517O1 on chromosome X (Corresponds to
the nucleic acid sequence of SEQ ID NO: 200)

L F S V L L R Y L A D N F L P G G S

SEQ ID NO: 49 Unknown protein from PAC clone RP5-1021I20 from 14q24.3 (Corresponds to
the nucleic acid sequence of SEQ ID NO: 201)

D W Q V L L G K L L W K I D N P G I

SEQ ID NO: 50 unknown protein from in DNA of chromosomes 8, 10, 14, 16 (Corresponds to
the nucleic acid sequence of SEQ ID NO: 202)

G A M E R E W A M F L R A A S S R I R G G V

SEQ ID NO: 51 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 203)

V H N F G R H W G L P L S F L L N Y P L F L S P

SEQ ID NO: 52 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 204)

A S M A P V G R D A E T L Q K Q K E T I K A F L K K L E A L M A S N D N A N K T

SEQ ID NO: 53 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 205)

C R E Q A E L T G L R L A S L G L K F N K I V H S S M T R A I E T

FIGURE 3B

SEQ ID NO: 54 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 206)

G T R I S D M L K L I A D T W Q R N C C P A

SEQ ID NO: 55 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 207)

E Q A S V K Y V I L D M Y R A L L T L M N T S T A T

SEQ ID NO: 56 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 208)

E D L E S V L I R L I N W A K G S P I P

SEQ ID NO: 57 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 209)

R P V S F C G A V W T L N R A I G R H F V R G S R

SEQ ID NO: 58 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 210)

H A V V A R L L H I G A I M F Q R L D F I E Q L S A P P A

SEQ ID NO: 59 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 211)

G Q G T L W G S G M E A W L A T V L K A L P W H P T Y Q L E P

SEQ ID NO: 60 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 212)

I A Q A T K A T I D K W N C I K L K I F Y T S K K E A S

SEQ ID NO: 61 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 213)

V V D V P D F I V W L E E A V S D L H R A L

SEQ ID NO: 62 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 214)

Q R R G N E F Q L R D L A D A W D L S S R S R Q R G W Q M P N C R S R R G P G

SEQ ID NO: 63 Proline/glutamine rich splicing factor (Corresponds to the nucleic acid
sequence of SEQ ID NO: 215)

R G L W V D R V L E E W G L E P R Q

FIGURE 3B

SEQ ID NO: 64 Transforming growth factor (Corresponds to the nucleic acid sequence of SEQ ID NO: 216)

FVRSVGVRLQNIGDDMDHAICGHDVRLG

SEQ ID NO: 65 L-plastin (Corresponds to the nucleic acid sequence of SEQ ID NO: 217)

--SGLRKPTCGSSQR

SEQ ID NO: 66 Arsenate resistance protein (Corresponds to the nucleic acid sequence of SEQ ID NO: 218)

AGTQPLILAQFMRVGGDELLHFLLW

SEQ ID NO: 67 K-Ras oncogene (Corresponds to the nucleic acid sequence of SEQ ID NO: 219)

MDTIKGFDLITNFQVVADALNISLLPNPLATA

SEQ ID NO: 68 Lysosomal pepstatin insensitive protease (Corresponds to the nucleic acid sequence of SEQ ID NO: 220)

ATWMKTLQGLLDRIQAFPSSPH

SEQ ID NO: 69 MYBPC3 (Corresponds to the nucleic acid sequence of SEQ ID NO: 221)

EANRKQPKPNNSSTAYYNFTGVSILPSYKP

SEQ ID NO: 70 cDNA FLJ20617 (Corresponds to the nucleic acid sequence of SEQ ID NO: 222)

GSLTHHINNIKPSSTR

SEQ ID NO: 71 UDP glucuronosyl transferase 2B4 precursor (Corresponds to the nucleic acid sequence of SEQ ID NO: 223)

VSCWPSYLYPLSTASASLLATQLKSIA

FIGURE 3C

SEQ ID NOS:72 and 153

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTACTTCACAATGGCTTCCATGA
GGCAGGCTGAACCTGCAGATATGCGCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTG
GAGACGAGTTTAAACGCCTACTATGCAAGGGAGGATTACAAAGACGATGACGATAAGGCATCCG
CTATTTAAAA

SEQ ID NOS:73 and 154

TACTATTTACAATTCTCCTAACACAATGGGGGCAGGTGGGGACGGCAGCTCGCCATCATCGGG
GACGACATCAACCGACGGAAGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:74 and 155

TTTACAATTCTCCTAACACAATGAAGCTGAGCGAGTGTCTCAAGCGCATCGGGGACGAACTGG
ACAGTAACATGGAGCTGCAGAGGATGATTGCCGCCGTGGACACAGACTCCCCCGAGATTACA
AAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:75 and 156

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTCTCTACAATGACAGGGAAGG
AAGCCATACTGCGGAGGCTGGTGGCCCTGCTGGAGGAGGAGGCAGAAGTCATTAACCAGAAGC
TGGCCTCGGACCCCGCCCTGCGCAGCAAGCTGGTCCGCCCTGTCTCCGACTCTTTCGCCCACC
TGGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAA

SEQ ID NOS:76 and 157

GACTCACTATAGGGACAATTACTATTTACAATTCTTACTTCCAACGAGGGATGCTCTACTACC
AGACAGAGAAATATGATTTGGCTATCAAAGACCTTAAAGAAGCCTTGATTGAGCTTCGAGGGA
ACAATGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAA

SEQ ID NOS:77 and 158

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGGTGGGGAAA
GTGATACTGACCCCCACTTCCAGGATGCGCTAATGCAGCTCGCCAAAGCTGTGGCAAGTGCTG
CAGCTGCCCTGGTCTCAAGGCCAAGAGTGTGGCCCAACGAGATTACAAAGACGATGACGATA
GGGCATCCGCTATTAAAA

SEQ ID NOS:78 and 159

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTCTCTACAATGGGAACACGCC
AAGACAGAATGTTTGAGACAATGGCGATTGAGATTGAACAACCTTTGGCAAGGCTTACAGGGG
TAAATGATAAAATGGCAGAATATACCAACGCTGATTACAAAGACGATGACGATAAGGCATCCG
CTATTTAAAA

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FIGURE 3C

SEQ ID NOS:79 and 160

CTATTTACAATTCTCCTAACACAATGGCGGTACAGGAGGATCCGGTGCAGCGGGAGATTCACC
AGGACTGGGCTAACCGGGAGTACATTGAGATAATCACCAGCAGCATCAAGAAAATCGCAGACT
TTCTCAACTCGTTCGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:80 and 161

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGCGACTCGAC
AGGCCTTAAATGAGATCTCGGCCCGGCACAGTGGGATCCAGCAGCTTGAACGCAGTATTCGTG
AGCTGCACGACATATTCACTTTCTGGCTACCGAAGTGCGAGATTACAAAGACGATGACGATA
AGGCATCCGCTATTAAAAA

SEQ ID NOS:81 and 162

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGATGTTCTCCG
ACATCTACGGGATCCGGGAGATCGCGGACGGGTTGTGCCTGGAGGTGGAGGGGAAGATGGTCA
GTAGGCCAGAGGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:82 and 163

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGTTTTGGCTGG
AAGAAAGGGACTTTGAGGCGGGTGTTTTTGAAGTAGAAGCAATTGTTAACAGCATCAAAAGAA
GCGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:83 and 164

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTACTTCAATACAATGAAATGGG
ACACAGACAATACTCTAGGGACAGAAATCTCTTGGGAGAATAAGTTGGCTGAAGGGTTGAAAC
TGACTCTTGATACCATATTTGTACATCACGTCCTGCATGCCCCACACGATTACAAAGACGATG
ACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:84 and 165

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGCGGGGGGCAG
TGTTCTCCCAGGATAAGGACGTCGTGCAGGAGGCCACAAAGGTGCTGAGGAATGCTGCCGACA
ACTTCTACATCAACGACAGGGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:85 and 166

GACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGACCGGTACAGGAGCAC
CCAGATTTCATAAAGGAAGTCCAGGAATTGAACTCAGCTCTACATCAATCGGACCTAATAGACA
TCTACAGAACTCTCCACCCCGCTGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAA
A

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FIGURE 3C

SEQ ID NOS:86 and 167

TTTACAATTCTCCTAACACAATGACAAAGAGCAATGAACTAACCCGGGCAGTAGAGGAACTAC
ACAAACTTTTGAAAGAAGCTAGGGAAGATTACAAAGACGATGACGATAAGGCATCCGCTATTT
AAAA

SEQ ID NOS:87 and 168

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGACCTACTGGA
ACCTGCTGCCCCCAAGCGGCCCATCAAAGAGGTGCTGACGGACATCTTTGCCAAGGTGCTGG
AGAAGGGCTGGGTGGACAGCCGCTCCATCCACGATTACAAAGACGATGACGATAAGGCATCCG
CTATTTAAAA

SEQ ID NOS:88 and 169

CTATTTACAATTCTCCTAACACTATGGACTATGAGATGCTCTTCAACTCCTTCAGGGATTACA
AAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:89 and 170

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGCCGGGGAGG
ACATGGAGATCAGCGTGAAGGAGTTGCGGACAATCCTCAATAGGATCATCAGCAAACACAAAG
ACCTGCGGACCGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:90 and 171

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGGACTAAGAG
AAGAAAGTGAAGAGTACATGGCTGCTGCTGATGAATACAATAGACTGAAGCAAGTGAAGCAAC
CTGCAGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:91 and 172

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGAAGGGCATCA
TCAGCAGGTTGATGTCCGTGGAGGAAGAAGTGAAGAGGGACCACGCAGAGATGCAAGCGGCTG
TGGACTCCAAACAGAAGATCATTGATGCCCAGGAGAAGCGCATTGCCTCGTTGGATGCCGCCA
ATGCCCGCCTCATGAGTGCCCTGACCCAGCTGAAAGAGAGGTACAGCATGCAAGCCCGTAACG
GCATCTCCCCACCAACCCCGCGGATTACAAAGACGATGACGATAAGGCATCCACTATTTAAA
AAA

SEQ ID NOS:92 and 173

TAATACGACTCACTATAGGGACAAATACTATTTACAATTCTCCTAACACAATGTGGGAACGGA
TTGAGGAAAGGCTGGCTTATATTGCTGATCACCTTGGCTTCAGCTGGACAGAATTAGCAAGAG
CGCTGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

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FIGURE 3C

SEQ ID NOS:93 and 174

TAATACGACTCACTATAGGGGACAATTACTATTTACAATTGCTTACTTCACAATGGCTCGGGG
AGACTTTGCCCAGGCTGCCCAGCAGCTGTGGCTGGCCCTGCGGGCACTGGGCCGGCCCCCTGCC
CACCTCCCACGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:94 and 175

TAATACGACTCACTATAGGGGACAATTACTATTTACAATTCTTTCTCTACAATGGTGGTGGATG
TGCCAGATTTTATAGTCTGGCTTGAGGAGGCAGTATCTGATTTACATAGGGCCCTCGATTACA
AAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:95 and 176

CTTTTACAATTCTCCTAACACAATGGGCTTTTTGGCTGCCGAGCAGGACATCCGAGAGGAAAT
CAGAAAAGTTGTACAGAGTTTAGAACAACAGCTCGAGAGGTTTAACTCTACTGCAAGGGGT
CCAGGATTACAAAGACGATGACGATAAGGCATCCGCTAAGNAAA

SEQ ID NOS:96 and 177

TTAATACGACTCACTATAGGGATTACTATTTACAATTCTTACTTCACAATGCTGGACCCTGTA
AAGGATGTTCTAATTCTTTCTGCTCTGAGACGAATGCTATGGGCTGCAGATGACTTCTTAGAG
GATTTGCCCTTTTGAGCAAATAGGGAATCTAAGGGAGGAAATTATCAACTGTGCACAAGCGGAT
TACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:97 and 178

TTCTATTTACAATTCTCCTAACACAATGGCCAACCTCCTACTCCTCATGGTACCCATTCTAAT
CGCAATGGCATTCTAATGCTTACCGAACGAAAAATTCTAGGCTATATACAACCACGCGATTA
CAAAGACGATGACGATAAGGCATCCGCTAAANAAA

SEQ ID NOS:98 and 179

AATTCTCCTAACACANTGCTCCGGCTAAATACTACCGTATGGCCCACCATAATTACCCCCATA
CTCCTTACACTATTCTCATCAACCAACCGACTAATCACCACCCGGGATTACAAAGACGATGAC
GATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:99 and 180

CTATTTACAATTCTCCTAACACAATGACCCTCTACCTAAAACTCACAGCCCTCGCTGTCACTT
TCCTAGGACTTCTAACAGCCCTAGACCTCAACTACCCAACCGATTACAAAGACGATGACGATA
AGGCATCCGCTATNAAAAA

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FIGURE 3C

SEQ ID NOS:100 and 181

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGCGGGCGTGT
TCTCAGCCGAGCCGTGCGCGTTTCCACAGACCCGTGCGAGCATGGTGTTTGCCAGGCACCTGC
GGGAGGTGGGAGACGAGTTCAGGAGCAGACATCTCAACTCCACGGACGACGCAGACGAGGATT
ACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:101 and 182

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGGCTTAAAC
TTGCCACAGTTGCTGCCAGTATGGACAGAGTGCCAAAGGTTACTCCCAGCAGTGCCATCAGCA
GCATAGCAAGAGAGAACCACGAACCAGAAAGATTGGGCTTAAATGGAATAGCAGAGACAACAG
ATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:102 and 183

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGATGCGGGATC
TCCCAGGACACTACTATGAAACGCTCAAATTCCTTGTTGGGCCATCTCAAGACCATCGCTGACC
ACCGCGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:103 and 184

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTAGGTGTGGATGTGTGG
GGGCCGCATGGAGGACATCCCCTGCTCCAGGGTGGGCCATATCTACAGGAAGTATGTGCCCTA
CAAGGTCCCGCCGGAGTCAGCCTGGCCCCGAACCTTAAGCGGGTGGCCGATTGGATGGATTA
CAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:104 and 185

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGCGCTTAGTT
GGATCGAAATGGACACCGAGATGGAGATGCTTCTGGCTAGATTTGCGAGAACCCAGGAGACC
TGCATTTAGACCACTCTGTCCATTTGTGTGCCACCCCGATTACAAAGACGATGACGATAAGG
CATCCGCTATTTAAAA

SEQ ID NOS:105 and 186

CTATTTACAATTCTCCTAACACAATGACCTCCACCCTACCACACATTCGAAGAACCCGTGATT
ACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:106 and 187

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGAACGGAAATC
TGTTGCTTCATTTCATCGCCGACAGTGATTACAAAGACGATGACGATAAGGCATCCGCTATTT
AAAA

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FIGURE 3C

SEQ ID NOS:107 and 188

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTACTTCGCCCTGGACGACATCG
AGTGGTTTGTGGCCCCGGCTGCAGAAGGCAGCCGAGGCTTTCAAGCAGCTGAACCAGCCCGAT
TACAAAGACCATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:108 and 189

TAATACGACTCCTATAGGGACAATTACTATTTACAATTCTTACTTCAATACAATGCGCACCCCT
GCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCCTACT
CCAATGGCTCAGACTGCACCCGCTGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTA
AAA

SEQ ID NOS:109 and 190

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACGCCAAAGCACAATGGC
TGTTATAATTAACGAATTATCTCAGCGTGACAGCTGTGGTCCTTTGAAAATTAGCTTGAATAA
CAAGATCCTGGTGTATGGTAATTTATTTTCTCTTTCACCCCGATTACAAAGACGATGACGA
TAAGGCATCCGCTATTTAAAA

SEQ ID NOS:110 and 191

CAATTCTCCTAACACGATGGGACTGGCTAAAAAAGTAAAAGGAACCCGGCAAATCTTACCCC
GCCTGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAAA

SEQ ID NOS:111 and 192

NATTTCTATTTACAATTCTCCTAACACAATGAGCTCACAGGCACTTAGAATCCATCAGTGGCT
CCATCTTTTCTCAGACTTCACCTCCACCGATTACAAAGACGATGACGATAAGGCATCCGCTNN
AAAAA

SEQ ID NOS:112 and 193

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGACCAACCCA
TAGGAAAATGGGAAAAGTTGTTCCCGTTACAACCTTTACAAAACGTTACAAATGCTCATGTCCC
AGATGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:113 and 194

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTACTTCACAATGGGGGTCTCTG
AGGCCGAGGGAACATTTCCCGCTCAGCACTTTCTTCTTGGGATAGCATCCCGTCTAAGAAGCG
TGGCTGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

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FIGURE 3C

SEQ ID NOS:114 and 195

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGAGGGCGCCCA
GATTCATAAAGCAAATATTGCTAGATCTAAAGAGAGAGATAGACTTCAATGTGAGATTAGTAG
AATACTTCAACCCACTATCAGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:115 and 196

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGATCGTGGCTA
TCATTGCTGGTCGCCCTTCGGATGTTGGGTGACCAGTTCAACGGAGAATTGGAAGCTTCTGCCA
AAAACGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:116 and 197

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAACCTGGCTTTGGC
CTATTACAGCAGCCGACAGTATGCTTCAGCACTGAAGCATATCGCTGAGATTATTGAGCGTGG
CATCCGCCAGCAGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:117 and 198

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACGATGGCTGCCATGT
TATTAGACAGAAGAGGAAGTGTGACCTCTGGATAAATGAGATGTCACTATTACATAAGA
TTGTTCAAGATGTATATGGAACCTCTACCCGCCCCACTCCGATTACAAAGACGATGACGATA
AGGCATCCGCTATTTAAAA

SEQ ID NOS:118 and 199

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGCCTTGGCAAT
ACAAACCGATAGCTGATCTTTACAGAGGGAGAGAGAGCCGTCCCTCTGCCCCCGGGATTACA
AAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:119 and 200

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGCTGTTCTCAG
TGTTGCTACGTTATTTGGCAGATAACTTTCTGCCAGGAGGATCCGATTACAAAGACGATGACG
ATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:120 and 201

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGATTGGCAGG
TGTTGCTAGGAAAACACTTTTGGAATAAGATAATCCGGGCATCGATTACAAAGACGATGACG
ATAGGCATCCGCTATTTAAAA

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FIGURE 3C

SEQ ID NOS:121 and 202

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGGTGCTATGG
AGAGAGAATGGGCGATGTTTCTCAGGGCTGCTTCAAGCAGGATTAGGGGTGGCGTGGATTACA
AAGACGATGACGATAAGGCATCCGCTGTTTAAAA

SEQ ID NOS:122 and 203

CTATTTACAATTCTCCTAACACAATGGTGCATAACTTTGGGAGACACTGGGGTCTGCCCTTGA
GTTTTCTTCTCAATTACCCTTTATTCTCAGTCCGGATTACAAAGACGATGACGATAAGGCAT
CCGCTATTAAAAA

SEQ ID NOS:123 and 204

TAATACGACTCACTATAGGAAATACTATTTACAATTCTTACTTCACAATGGCTAGCATGGCTC
CAGTGGGGAGAGATGCAGAAACATTGCAAAAGCAAAAGGAACTATAAAAGCCTTTCTAAAGA
AACTAGAAGCCCTCATGGCAAGCAATGACAATGCCAATAAAACCGATGACAAAGACGATGACG
ATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:124 and 205

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGTGTGGGAGC
AGGCTGAACTCACTGGGCTCCGCCTGGCAAGCTTGGGGTTGAAGTTTAATAAAATCGTCCATT
CGTCTATGACGCGCGCCATAGAGACCACCGATTACAAAGACGATGACGATAAGGCATCCGCTA
TTTAAAA

SEQ ID NOS:125 and 206

TAATACGACTCACTATAGGGGACAATTACTATTTACAATTCTTACTTCACAATGGGCACTAGA
ATTAGTGATATGCTAAAAATTAATTGCAGACACATGGCAGAGAAATTGTTGCCCTGCGGATTAC
AAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:126 and 207

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGAGCAGGCCA
GTGTTAAGTATGTTATTCTGGATATGTACAGAGCACTCTTGACACTAATGAATACTTCAACAG
CCACAGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:127 and 208

CAATTCTCCTAACACAATGGAAGACCTAGAGAGTGTGTTAATAAGACTGATCAACTGGGCAAA
AGGAAGCCCCATCCAGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

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FIGURE 3C

SEQ ID NOS:128 and 209

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGAGGCCGGTGT
CCTTTTGCGGGGCTGTTTGGACTCTGAACAGGGCAATAGGAAGGCATTTTGTCCGAGGTAGCA
GGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:129 and 210

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGCACGCGGTGG
TGGCACGTTTGCTTCACATTGGGGCAATCATGTTCCAACGACTAGACTTCATAGAACAATTGT
CTGCACCCCCAGCGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:130 and 211

CTTTTACAATTCTCCTAACACAATGGGGCAAGGTACACTTTGGGGAAGTGGGATGGAAGCATG
GTTGGCAACGGTGTTGAAGGCACTCCCTTGGCACCCACATACCAGCTGGAGCCGGATTACAA
AGACGATGACGATAAGGCATCCGCTATANAAAA

SEQ ID NOS:131 and 212

TTCTATTTACAATTCTCCTAACACAATGATAGCACAGGCAACGAAAGCAACAATAGACAAATG
GAACTGCATCAAACCTTAAAATCTTCTACACCTCAAAGAAAGAAGCCAGCGATTACAAAGACGA
TGACGATAAGGCATCCGCTANT

SEQ ID NOS:132 and 213

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGTGGTGGATG
TGCCAGATTTTATAGTCTGCTTGAGGAGGCAGTATCTGATTTACATAGAGCCCTCGATTACA
AAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:133 and 214

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGCAGAGGAGAG
GGAATGAATTCCAGCTGAGAGACCTGGCCGATGCATGGGATTTGTCTTCAAGGTCCAGGCAGA
GGGGATGGCAGATGCCAAATTGCAGAAGTCGAAGAGGGCCCCGAGATTACAAAGACGATGACG
ATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:134 and 215

TTTACAATTCTCCTAACACAATGCGGGGCGCTGTGGGTGGACAGGGTCCTAGAGGAATGGGGCC
TGGAACCGCGGCAGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAAA

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FIGURE 3C

SEQ ID NOS:135 and 216

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTACTCTACAATGTTTCGTGAGG
TCTGTTGGCTGGAGGCTGCAGAACATTGGTGATGACATGGACCACGCCATTTGTGGCCATGAT
GTCAGGCTCGGCGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:136 and 217

GCAGTGGACTCAGAAAGCCAACATGTGGCTCCTCCCAGCGCGATTACAAAGACGATGACGATA
AGGCATCCGCTATTTAAAA

SEQ ID NOS:137 and 218

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGCGGGTACAC
AGCCACTTATCCTTGCCAGTTTCATGCGTGTTGGAGGTGACGAACCTCTCCACTTCCTGCTCT
GGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:138 and 219

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACCATGATGGATACCA
TAAAGGGATTGACCTAATCACTAATTTTCAGGTGGTGGCTGATGCTTTGAACATCTCTTTGC
TGCCCAATCCATTAGCGACAGCGGATTACAAAGACGATGACGATAAGGCATACGCTATTTAAA
A

SEQ ID NOS:139 and 220

TCTATTTACAATTCTCCTAACACAATGGCCACTTGGATGAAAACCCTTCAAGGATTACTGGAT
AGAATTCAGGCTTTCCCTCCAGCCCCACGATTACAAAGACGATGACGATAAGGCATCCGCT
ANGAAAAAA

SEQ ID NOS:140 and 221

CTATTTACAATTCTCCTAACACAATGGAAGCTAATAGAAAACAACCGAAACCAATAATTCAA
GCACTGCTTATTACAATTTTACTGGGGTCTCTATTTTACCCTCCTACAAGCCCCAGATTACAA
AGACGATGACGATAAGGCATCCGCTATAAAAAA

SEQ ID NOS:141 and 222

TTCTATTTACAATTCTCCTAACACAATGGGGCTCACTCACCCACCACATTAACAACATAAAAC
CCTCATCCACACGAGATTACAAAGACGATGACGATAAGGCATCCGCTANAAAAAA

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FIGURE 3C

SEQ ID NOS:142 and 223

TAATACGACTCATATAGGGACAATTACTATTTACAATTCTTACTTCACAATGGTGAGCTGCTG
GCCGATTACTAAAATACCCTTTGTCTACAGCCTCCGCTTCTCTCCTGGCTACGCAATTGAAAA
GCATAGCGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAAAA

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A. BimL

10 20 30 40 50 60 70 80 90 100 110 120 130
MAKOPSDVSECDREGQLOPAERPPQLRFGAPTSLOTEPODRSPAPMSCDKSTQTPSPCQAFNHYSASAMRQAEPADMRPEITIAQELRRICDEFNAYYARRVFLNNYQAAEDHPRVILRLRYIVRLWEMH
1 P57-V107
1 A72-H118
3 -A115
1 -A114
16 -V107
20 -R106
7 R75-S120*
2 -P199*
1 -H118
1 -A115
4 -V107
9 -R106
5 Q76-R106

B. Bax

10 20 30 40 50 60 70 80 90 100 110 120 210
MDGSGEQPRGGPTSSSEQIMKYGALLQGTQDRAGMGEAPELADPTQDAATKLSCLRIQDELDENMLQPMIAADTSPREVFYVADMFSDGNFNGRVVALFYFASKVLKA // DVYINAFSLRY
1 G39-M86*
1 -R89
1 -D84
1 -V83
1 -A82
1 -Q77
1 D48-R89
1 -V83
13 K58-H118

C. HSPC300

10 20 30 40 50 60 70 80 90 100
MGAAMAGQEDPVQREXHOEWANREYIEITSSIKKIADFLNSFDMSCRSRLATNEKLTALERIEYIEARVTKGETLITRTPCCCEVALHNTGHMGKAPAFSFLSP
11 G2-F43
6 -S42
13 A6-F43
4 -S42

D. TPR

10 280 290 300 310 320 330 340 350 360 370 2340
MAAVLQQVLE // NAHIKLSNLYKSAADDSKSNELTRAVEELHKLKEAGEANKAIQDHLLVEQSKDQWEREMLEKIGRLEKELNANDLLSATKKEGALLSEELAAKMSPT // RGINRGININ
19 D294-P322*
2 A298-E319

FIGURE 4

20200505/2600T

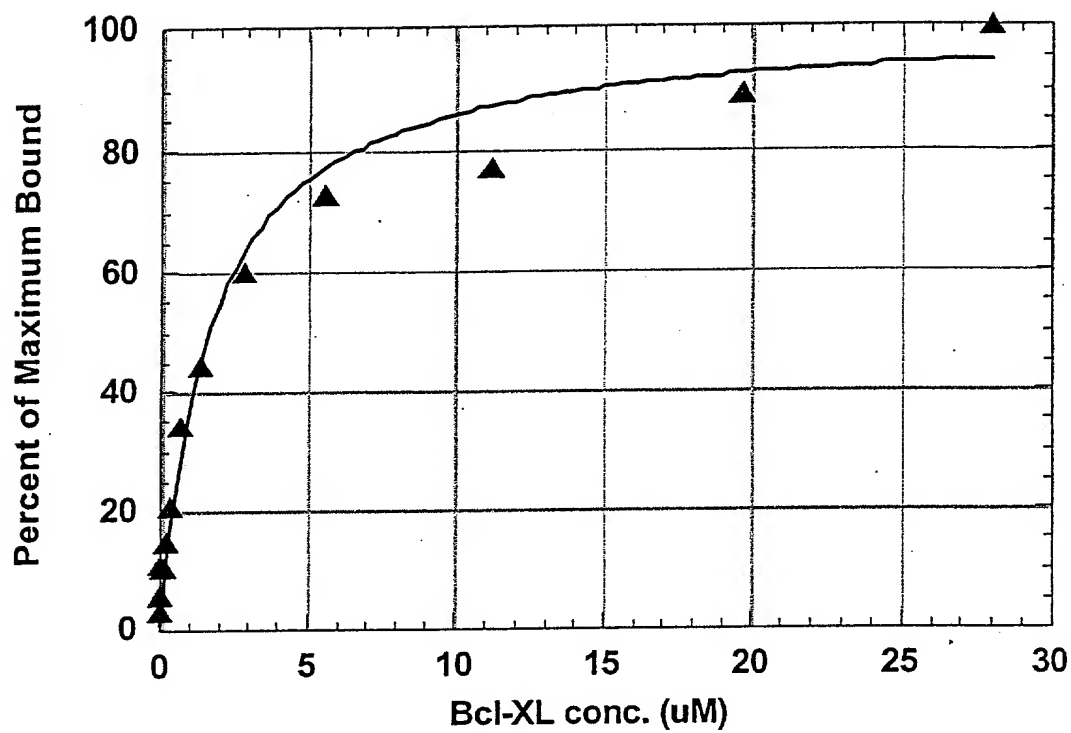


FIGURE 5

2020052500T

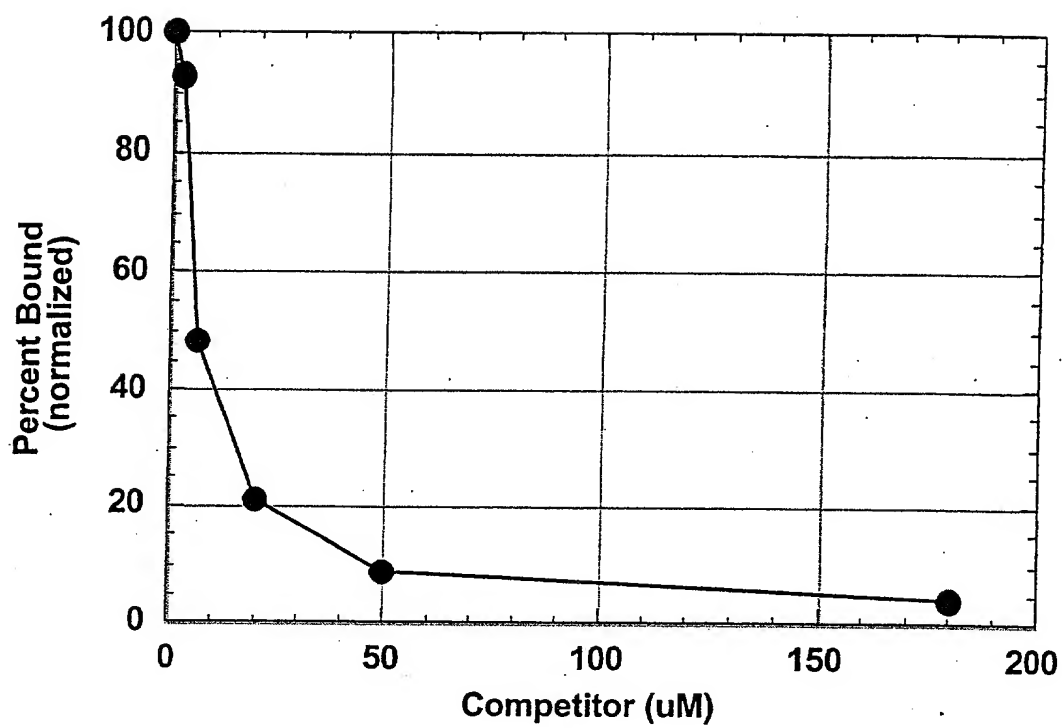


FIGURE 6

Number	Protein Name	Accession number	Clone	Protein Sequence
224	Cdc21	CAA52801	AtB-Br-M39	KYQQLFEDIRW
225	SRP9	NP_003124	AtB-Hc-8	IGEEFSRAAEKLYLAV
226	Bmf	NP_277038	AtB-Thy-34	KAEVQIARKLQCIADQFHRLHVL
227	Unknown protein from human chromosome 2 clone RP11-228G11	AC098559	AtB-Br-M45	MGDVVGFIDELEGAVSDLHRAL
228	Unknown protein from human chromosome 14 clone CTD-3014H8 and RP11-285P	AC007955	AtB-Thy-38	TLRHWGLQFNTRFGV
229	Sequence/protein not in database	none	AtB-BM-51	SRREEAWDALFRGI
230	Sequence/protein not in database	none	AtB-BM-52	TLREIGDLYLTSILGRR

Figure 8A

202050.05225007

SEQ ID NO: 224 Cdc21 (Corresponds to nucleic acid sequence of SEQ ID NO: 231)

KYQQLFEDIRW

SEQ ID NO: 225 SRP9 (Corresponds to nucleic acid sequence of SEQ ID NO: 232)

IGEEFSRAAEKLYLAV

SEQ ID NO: 226 Bmf (Corresponds to nucleic acid sequence of SEQ ID NO: 233)

KAEVQIARKLQCIADQFHRLHVL

SEQ ID NO: 227 Unknown protein from human chromosome 2 clone RP11-228G11 (Corresponds to nucleic acid sequence of SEQ ID NO: 234)

MGDVVGFIDELEGAVSDLHRAL

SEQ ID NO: 228 Unknown protein from human chromosome 14 clone CTD-3014H8 and RP11-285P (Corresponds to nucleic acid sequence of SEQ ID NO: 235)

TLRHWGLQFNTRFGV

SEQ ID NO: 229 Sequence/protein not in database (Corresponds to nucleic acid sequence of SEQ ID NO: 236)

SRREEAWDALFRGI

SEQ ID NO: 230 Sequence/protein not in database (Corresponds to nucleic acid sequence of SEQ ID NO: 237)

TLREIGDLYLTSILGRR

Figure 8B

SEQ ID NO: 231

AAATACCAGCAACTTTTTGAAGATATTCGGTGG

SEQ ID NO: 232

ATCGGGGAGGAGTTCAGCCGCGCTGCCGAGAAGCTTTACCTCGCTGTT

SEQ ID NO: 233

AAAGCAGAGGTACAGATTGCCCCGAAAGCTTCAGTGCATTGCAGACCAAGTTC
CACCGGCTTCATGTGCTT

SEQ ID NO: 234

ATGGGAGATGTGGTTGGTTTTATAGACGAACTTGAGGGGGCAGTGTCTGAT
TTACATAGGGCGTTG

SEQ ID NO: 235

ACACTCCGACACTGGGGATTACAGTTCAACACAAGATTTGGTGTG

SEQ ID NO: 236

TCGAGAAGGGAAGAGGCATGGGATGCTTTATTTTCGTGGGATC

SEQ ID NO: 237

TCGAGAAGGGAAGAGGCATGGGATGCTTTATTTTCGTGGGATC

Figure 8c

2040E0.052600T

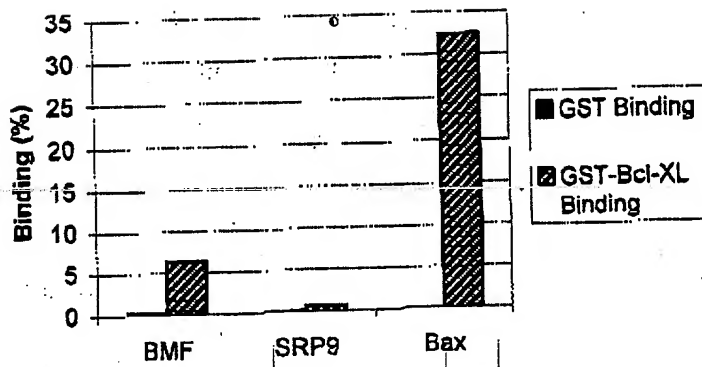


Figure 9

SRP9

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SRP9

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